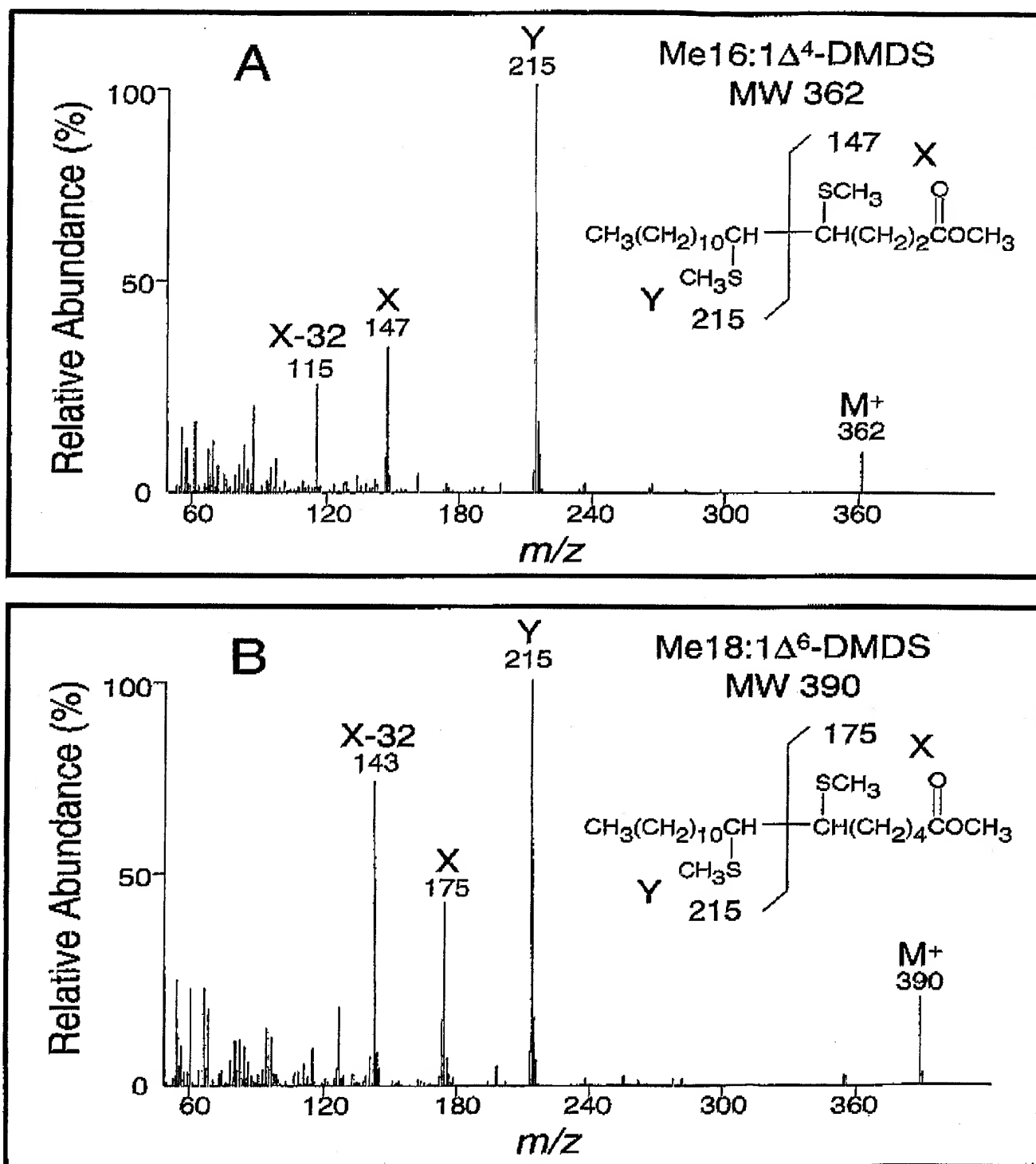


## APPENDIX A



## APPENDIX B

## #NEXUS

[!Alignment of:]

```
[Sequence      Start   End   Sequencetype]
[SEQ ID NO 6   (1 >   137)   PROTEIN]
[SEQ ID NO 2   (1 >   394)   PROTEIN]
[417819        (1 >   385)   PROTEIN]
[A47245        (1 >   385)   PROTEIN]
```

begin data;

dimensions ntax=4 nchar=398;

format datatype=Protein interleave gap=- missing='.';

matrix

```
SEQ ID NO 6  MA-----SVTASSISFTSI--ASSLKQ
SEQ ID NO 2  MALKLN---FQCKKNHPAAFAKSPLFVTRVSSPRVFMASVNSNSMVLNLIKSPPNLQV
417819       MAMKLNALMTLQCPKRN--MFTRIAPPQAGRVRSKVSMASLHASPLVFDKLGKAGR----
A47245       MAMKLNALMTLQCPKRN--MFTRIAPPQAGRVRSKVSMASLHASPLVFDKLGKAGR----
```

```
SEQ ID NO 6  NQGLAKSSISL--SVNG-----KSFRRS---
SEQ ID NO 2  THSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRRERAK
417819       -----PEVDELFNSLEGWARDNIIHLKSVENSWQPQDYLPDPTSDAFEDQVKEMRRERAK
A47245       -----PEVDELFNSLEGWARDNIIHLKSVENSWQPQDYLPDPTSDAFEDQVKEMRRERAK
```

```
SEQ ID NO 6  -----
SEQ ID NO 2  EIPDDYFVVLVGDMITEEALPTYMSMLNRCDBGIKDETGAEPSAWAMWTRAWTAEENRHGD
417819       DIPDEYFVVLVGDMITEEALPTYMSMLNRCDBGIKDDTGAQPTSWATWTRAWTAEENRHGD
A47245       DIPDEYFVVLVGDMITEEALPTYMSMLNRCDBGIKDDTGAQPTSWATWTRAWTAEENRHGD
```

```
SEQ ID NO 6  -----LRLLSAPLRFVRVSCAAKPAT-----
SEQ ID NO 2  LLNKYLVLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFITYTSFQERATFISHANTAK
417819       LLNKYLVLSGRVDMRMIEKTIQYLIGSGMDTKTENC PYMGFIYTSFQERATFISHANTAK
A47245       LLNKYLVLSGRVDMRMIEKTIQYLIGSGMDTKTENC PYMGFIYTSFQERATFISHANTAK
```

```
SEQ ID NO 6  -----VDKVC-----EIVRKQLALPAD
SEQ ID NO 2  LAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAIEDPDTTVIAFADMMRKKIQMPAH
417819       LAQHYGDKNLAQVCGNIASDEKRHATAYTKIVEKLAIEDPDTTVIAFSDMMRKKIQMPAH
A47245       LAQHYGDKNLAQVCGNIASDEKRHATAYTKIVEKLAIEDPDTTVIAFSDMMRKKIQMPAH
```

```
SEQ ID NO 6  SAVTGESK-----FAALGAD-----SLDTVEIVMGLEEEF-----GISVEEESAQT-IA
SEQ ID NO 2  LMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQYVC
417819       AMYDGSDDMLFKHFTAVAQQIGVYSAWDYCDIIDFLVDKWNVAKMTGLSGEGRKAQYVC
A47245       AMYDGSDDMLFKHFTAVAQQIGVYSAWDYCDIIDFLVDKWNVAKMTGLSGEGRKAQYVC
```

```
SEQ ID NO 6  TVQDAADLIEKLVEKKE-----
SEQ ID NO 2  ELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
417819       SLAAKIRRVEEKVQGKEKK--AVLEPAFWSWIFNRQIII
A47245       SLAAKIRRVEEKVQGKEKK--AVLEPAFWSWIFNRQIII
```

Pair Distances of Untitled ClustalV (PAM250)

Percent Similarity in upper triangle

Percent Divergence in lower triangle

	SEQ ID NO 6	SEQ ID NO 2	417819	A47245	
SEQ ID NO 6	***	14.6	14.6	14.6	SEQ ID NO 6
SEQ ID NO 2	232.0	***	73.8	73.8	SEQ ID NO 2
417819	191.3	26.6	***	100.0	417819